



CRISPR Interference Efficiently Induces Specific and Reversible Gene Silencing in Human iPSCs.

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Public Summary:

Developing technologies for efficient and scalable disruption of gene expression will provide powerful tools for studying gene function, developmental pathways, and disease mechanisms. Here, we develop clustered regularly interspaced short palindromic repeat interference (CRISPRi) to repress gene expression in human induced pluripotent stem cells (iPSCs). CRISPRi, in which a doxycycline-inducible deactivated Cas9 is fused to a KRAB repression domain, can specifically and reversibly inhibit gene expression in iPSCs and iPSC-derived cardiac progenitors, cardiomyocytes, and T lymphocytes. This gene repression system is tunable and has the potential to silence single alleles. Compared with CRISPR nuclease (CRISPRn), CRISPRi gene repression is more efficient and homogenous across cell populations. The CRISPRi system in iPSCs provides a powerful platform to perform genome-scale screens in a wide range of iPSC-derived cell types, dissect developmental pathways, and model disease.

Scientific Abstract:

Developing technologies for efficient and scalable disruption of gene expression will provide powerful tools for studying gene function, developmental pathways, and disease mechanisms. Here, we develop clustered regularly interspaced short palindromic repeat interference (CRISPRi) to repress gene expression in human induced pluripotent stem cells (iPSCs). CRISPRi, in which a doxycycline-inducible deactivated Cas9 is fused to a KRAB repression domain, can specifically and reversibly inhibit gene expression in iPSCs and iPSC-derived cardiac progenitors, cardiomyocytes, and T lymphocytes. This gene repression system is tunable and has the potential to silence single alleles. Compared with CRISPR nuclease (CRISPRn), CRISPRi gene repression is more efficient and homogenous across cell populations. The CRISPRi system in iPSCs provides a powerful platform to perform genome-scale screens in a wide range of iPSC-derived cell types, dissect developmental pathways, and model disease.

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